

SEQUENCE LISTING

<110> Novozymes A/S

<120> Protease Variants

<130> 10517.000-DK

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<170> PatentIn Ver. 2.1

<210> 1

<211> 948

<212> DNA

<213> Bacillus licheniformis

<220>

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<221> mat_peptide

<222> (283)..(948)

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<221> sig_peptide

<222> (1)..(90)

<223> pro_peptide (914) ... (282)

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ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca	96
Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro	
-75 -70 -65	
tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca	144
Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr	
-60 -55 -50	
tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat	192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr	
-45 -40 -35	
tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa	240
Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys	
-30 -25 -20 -15	
gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg	288
Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val	
-10 -5 -1 1	
att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg	336
Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro	
5 10 15	
tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga	384
Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly	

20	25	30	
tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat			432
Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr	40	45	50
gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga			480
Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly	55	60	65
cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac			528
Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr	70	75	80
ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga			576
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly	85	90	95
gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga			624
Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly	100	105	110
tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc			672
Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser	115	120	125
ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga			720
Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly	135	140	145
ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg			768
Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr	150	155	160
tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga			816
Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg	165	170	175
acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta			864
Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val	180	185	190
tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg			912
Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val	195	200	205
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Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln	215	220	

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<211> 316

<212> PRT

<213> Bacillus licheniformis

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-85

-80

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-75

-70

-65

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr

-60

-55

-50

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-45

-40

-35

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
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 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
 20 25 30
 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 35 40 45 50
 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 55 60 65
 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
 70 75 80
 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 85 90 95
 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
 100 105 110
 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
 115 120 125 130
 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 135 140 145
 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
 150 155 160
 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 165 170 175
 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
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 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
 195 200 205 210
 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
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 <213> Bacillus halmapalus AA513

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 <222> (1)..(78)
 <223> Pro-peptide (79) ... (360)

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 ggg att cta tcc cca gta aac gca act caa gct gag act ctt act aaa 96
 Gly Ile Leu Ser Pro Val Asn Ala Thr Gln Ala Glu Thr Leu Thr Lys
 -100 -95 -90
 tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat gaa 144
 Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp Glu
 -85 -80 -75
 gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg att 192
 Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser Ile
 -70 -65 -60
 att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act tct 240
 Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr Ser
 -55 -50 -45
 tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa gaa 288
 Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu Glu
 -40 -35 -30 -25
 ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag cct 336
 Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys Pro
 -20 -15 -10
 att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg aga 384
 Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly Arg
 -5 -1 1 5
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 10 15 20
 att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt gtg 480
 Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly Val
 25 30 35 40
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 Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly Ser
 45 50 55
 gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg gca 576
 Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp Ala
 60 65 70
 tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac aga 624
 Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr Arg
 75 80 85
 aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca cct 672
 Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala Pro
 90 95 100
 gac tct gat gga cgt cat att gga aac aga gct gga att tta tct ttt 720
 Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser Phe
 105 110 115 120
 aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat gga 768
 Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr Gly
 125 130 135
 tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg gga 816
 Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp Gly

140										145				150				
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Met	Val	Gly	Arg	Ser	Asp	Ala	Phe	Leu	His	Arg	Asp	Leu	Leu	Phe	Tyr			
		155					160					165						
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Asn	Met	Asp	Thr	Tyr	Phe	Gly	Gln	Ser	Gly	Ser	Pro	Val	Leu	Asn	Ser			
	170					175					180							
gta	gat	tca	atg	ggt	gca	ggt	cat	aat	gca	ggg	tat	atc	ggt	ggt	ggt	960		
Val	Asp	Ser	Met	Val	Ala	Val	His	Asn	Ala	Gly	Tyr	Ile	Val	Gly	Gly			
185					190					195					200			
aat	agg	gaa	att	aat	ggt	ggt	cct	aaa	atc	aga	aga	gat	ttt	aca	aac	1008		
Asn	Arg	Glu	Ile	Asn	Gly	Gly	Pro	Lys	Ile	Arg	Arg	Asp	Phe	Thr	Asn			
				205					210					215				
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Leu	Phe	Asn	Gln	Met	Asn													
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 <213> Bacillus halmapalus AA513

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 Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp Glu
 -85 -80 -75
 Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser Ile
 -70 -65 -60
 Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr Ser
 -55 -50 -45
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 -40 -35 -30 -25
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 -20 -15 -10
 Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly Arg
 -5 -1 1 5
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 10 15 20
 Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly Val
 25 30 35 40
 Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly Ser
 45 50 55
 Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp Ala
 60 65 70
 Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr Arg
 75 80 85

Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala Pro
 90 95 100
 Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser Phe
 105 110 115
 Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr Gly
 125 130 135
 Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp Gly
 140 145 150
 Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe Tyr
 155 160 165
 Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn Ser
 170 175 180
 Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly Gly
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 <212> DNA
 <213> Bacillus licheniformis AC116

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 -75 -70 -65
 ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144
 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
 -60 -55 -50 -45
 tat gat ccc aac ata aaa att gac aat aac ggc gca tat tcg aaa gcc 192
 Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
 -40 -35 -30
 ttc gaa gga acc gga aca ccc ggc ggc tcc gtt cag gcc aaa ccg aaa 240
 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15

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Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly	
-10 -5 -1 1	
tca gat gaa cgg aca agg gtg act gat aca acg gcc ttt cca tac aga	336
Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg	
5 10 15 20	
gca atc gtc cat att tca agc agc atc ggc tca tgc aca ggc tgg ctg	384
Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu	
25 30 35	
atc gga ccg aaa acg gta gca acg gcc ggg cac tgc gtc tat gac acg	432
Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr	
40 45 50	
gca agc cga tca ttc gcg gga acc gcc acc gtt tcc ccg gga cga aac	480
Ala Ser Arg Ser Phe Ala Gly Thr Thr Val Ser Pro Gly Arg Asn	
55 60 65	
ggt tca gct tac cct tac gga tct gtt aca tcg acc cgc tat ttc atc	528
Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile	
70 75 80	
ccg tcg ggt tgg cag agc gga aat tcc aat tat gac tac gca gcg atc	576
Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile	
85 90 95 100	
gag ctc agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca	624
Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser	
105 110 115	
tac acc gct tca tcg ctt gca gga gca ggc gtg acc atc agc gga tat	672
Tyr Thr Ala Ser Ser Leu Ala Gly Gly Val Thr Ile Ser Gly Tyr	
120 125 130	
cca gga gac aaa aca aca ggc acc cag tgg caa atg tcc gga acg atc	720
Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile	
135 140 145	
gct gtt tca gaa acg tat aaa ctg caa tat gcg atc gac aca tac gga	768
Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly	
150 155 160	
ggt caa agc ggt tcc ccg gta tat gag aaa agc agt tca agg aca aac	816
Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn	
165 170 175 180	
tgc agc ggc cca tgc tcg ctg gcc gtt cat acg aac ggc gtg tac gga	864
Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly	
185 190 195	
gga tcc tct tac aac aga ggc acc cgc att acg aaa gaa gta ttt gat	912
Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp	
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<212> PRT

<213> Bacillus licheniformis AC116

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 -40 -35 -30
 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15
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 -10 -5 -1 1
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 5 10 15 20
 Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
 25 30 35
 Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
 40 45 50
 Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
 55 60 65
 Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
 70 75 80
 Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
 85 90 95 100
 Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
 105 110 115
 Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
 120 125 130
 Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
 135 140 145
 Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
 150 155 160
 Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn
 165 170 175 180
 Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
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<223> pro-peptide (79) ... (264)

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gct tta agt gtg cct agt ttt gcc cat gcc gca tct gat tca gtg cta	96
Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu	
-70 -65 -60	
acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca	144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser	
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agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gat aaa gtg	192
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val	
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gat gat cta tct tca act gtt ggt gaa aaa gta aaa cca cta tca aaa	240
Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys	
-20 -15 -10	
tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat ggt aga	288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg	
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aca aaa gta gca aat aca aga gtg gca cca tat aat tca att gct tat	336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr	
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act acg ttt ggc ggc tcc agc tgc acg ggg acc ctg att gcc cct aac	384
Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn	
25 30 35 40	
aaa att ttg aca aac gga cac tgc gtg tac aat aca gca tcc aga agt	432
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser	
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tat agt gca aaa gga tcg gtg tat cca ggc atg aat gat agt act gcg	480
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala	
60 65 70	
gtg aat ggc tca gca aat atg aca gag ttc tat gta cca agc ggg tat	528
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr	
75 80 85	
atc aat aca ggt gcg agc caa tat gat ttt gcc gtg atc aaa aca gat	576
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp	
90 95 100	
acg aac att ggc aat aca gtt ggt tac cgt tcc atc cgt cag gtg aca	624
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr	
105 110 115 120	
aac tta act ggg aca acg att aaa att tct gga tat cca ggt gat aaa	672
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys	
125 130 135	

atg	aga	tca	act	ggc	aag	atc	tcg	cag	tgg	gag	atg	tca	ggg	cct	gtg	720
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Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Met	Ile	Asp	Thr	Phe	Ser	
		155					160					165				
gga	aat	tca	ggc	tca	gcg	atg	cta	gat	caa	aat	cag	caa	att	gtt	ggg	816
Gly	Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly	
		170				175					180					
gtt	cat	aac	gca	ggg	tat	tca	aac	ggg	acg	att	aat	ggc	ggg	cca	aaa	864
Val	His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys	
185					190					195					200	
gcg	aca	gct	gcc	ttt	gtt	gaa	ttt	atc	aac	tat	gca	aaa	gcg	caa		909
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 Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
 -40 -35 -30 -25
 Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
 -20 -15 -10
 Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg
 -5 -1 1 5
 Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
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 Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
 25 30 35 40
 Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
 45 50 55
 Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
 60 65 70
 Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
 75 80 85
 Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
 90 95 100
 Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
 105 110 115 120
 Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
 125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val
 140 145 150
 Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
 155 160 165
 Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
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 Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
 185 190 195 200
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 205 210 215

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 Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
 -80 -75 -70 -65
 cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca 144
 His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
 -60 -55 -50
 agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa 192
 Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
 -45 -40 -35
 gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa 240
 Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
 -30 -25 -20
 agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa 288
 Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
 -15 -10 -5 -1
 tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca 336
 Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
 1 5 10 15
 tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc 384

Tyr	Pro	Tyr	Arg 20	Ala	Ile	Val	His	Ile 25	Ser	Ser	Ser	Ile	Gly 30	Ser	Cys	
acc	ggc	tcc	ctg	atc	ggc	ccg	aaa	acg	gtg	gca	acg	gcc	gga	cac	tgc	432
Thr	Gly	Ser 35	Leu	Ile	Gly	Pro	Lys 40	Thr	Val	Ala	Thr	Ala 45	Gly	His	Cys	
att	tat	gac	aca	gcg	agc	ggg	tca	ttc	gcc	gga	acc	gct	acc	gtt	tct	480
Ile	Tyr 50	Asp	Thr	Ala	Ser	Gly 55	Ser	Phe	Ala	Gly	Thr 60	Ala	Thr	Val	Ser	
ccg	gga	cgg	aac	ggc	tca	aca	tat	ccg	tac	gga	tca	gtt	aca	tca	acc	528
Pro 65	Gly	Arg	Asn	Gly	Ser 70	Thr	Tyr	Pro	Tyr	Gly 75	Ser	Val	Thr	Ser	Thr 80	
cgc	tat	ttc	atc	ccg	tca	ggc	tat	cga	agc	gga	aat	tcg	aat	tac	gac	576
Arg	Tyr	Phe	Ile	Pro 85	Ser	Gly	Tyr	Arg	Ser 90	Gly	Asn	Ser	Asn	Tyr 95	Asp	
tac	gga	gcc	ata	gag	ctc	agc	cag	ccg	atc	ggc	aac	acc	gtc	ggg	tat	624
Tyr	Gly	Ala	Ile 100	Glu	Leu	Ser	Gln	Pro 105	Ile	Gly	Asn	Thr	Val 110	Gly	Tyr	
ttc	gga	tat	tcc	tac	acc	acc	tcg	tct	ctc	gtt	ggg	tca	agc	gtt	acc	672
Phe	Gly	Tyr 115	Ser	Tyr	Thr	Thr	Ser 120	Ser	Leu	Val	Gly	Ser 125	Ser	Val	Thr	
atc	atc	gga	tat	cca	ggc	gac	aaa	aca	tcg	ggc	acc	caa	tgg	cag	atg	720
Ile	Ile 130	Gly	Tyr	Pro	Gly	Asp 135	Lys	Thr	Ser	Gly	Thr 140	Gln	Trp	Gln	Met	
tcc	gga	aat	atc	gcc	gtc	tca	gaa	aca	tat	aaa	ctg	caa	tat	gcg	atc	768
Ser 145	Gly	Asn	Ile	Ala	Val 150	Ser	Glu	Thr	Tyr	Lys 155	Leu	Gln	Tyr	Ala	Ile 160	
gac	aca	tac	gga	ggg	cag	agc	ggc	tct	ccc	gta	tat	gag	gcg	agc	agc	816
Asp	Thr	Tyr	Gly 165	Gly	Gln	Ser	Gly	Ser	Pro 170	Val	Tyr	Glu	Ala	Ser 175	Ser	
tcc	aga	acg	aat	tgc	agc	ggc	cca	tgt	tcg	ctg	gcc	gtt	cat	acg	aat	864
Ser	Arg	Thr	Asn 180	Cys	Ser	Gly	Pro	Cys 185	Ser	Leu	Ala	Val	His 190	Thr	Asn	
ggg	gtg	tac	gga	gga	tct	tca	tac	aac	aga	ggc	acc	cgg	att	aca	aaa	912
Gly	Val	Tyr 195	Gly	Gly	Ser	Ser	Tyr 200	Asn	Arg	Gly	Thr	Arg 205	Ile	Thr	Lys	
gaa	gta	ttc	gat	aat	ttg	aca	aac	tgg	aaa	aac	agc	gcc	caa			954
Glu	Val 210	Phe	Asp	Asn	Leu	Thr 215	Asn	Trp	Lys	Asn	Ser 220	Ala	Gln			

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 -95 -90 -85
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 -80 -75 -70 -65
 His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
 -60 -55 -50
 Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys

-45 -40 -35
 Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
 -30 -25 -20
 Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
 -15 -10 -5 -1
 Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
 1 5 10 15
 Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
 20 25 30
 Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
 35 40 45
 Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
 50 55 60
 Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
 65 70 75 80
 Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
 85 90 95
 Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
 100 105 110
 Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
 115 120 125
 Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
 130 135 140
 Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
 145 150 155 160
 Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser
 165 170 175
 Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn
 180 185 190
 Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys
 195 200 205
 Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 210 215 220

<210> 11
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 <212> DNA
 <213> Bacillus pumilus JA96

<220>
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<223> pro-peptide (76) ... (261)

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tta	agt	gtg	cct	agt	ttt	gcc	cat	gca	gca	tct	gat	tca	gta	ctt	acg	96
Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Ala	Ser	Asp	Ser	Val	Leu	Thr	
	-70					-65					-60					
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Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser	Ala	
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Asp	Phe	His	Asn	Asp	Met	Lys	Thr	Pro	Ser	Ser	Phe	Asp	Lys	Val	Asp	
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gat	ctc	tct	tct	act	att	ggc	gaa	aaa	gta	aaa	cca	ctc	aca	aca	tat	240
Asp	Leu	Ser	Ser	Thr	Ile	Gly	Glu	Lys	Val	Lys	Pro	Leu	Thr	Thr	Tyr	
			-20					-15					-10			
tta	aaa	gac	ttt	caa	aca	aaa	gta	gtc	att	gga	gac	gat	ggg	aga	aca	288
Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Arg	Thr	
		-5				-1	1			5						
aaa	gtg	acg	aat	aca	aga	gta	gca	ccc	tat	aat	tct	att	gct	tat	att	336
Lys	Val	Thr	Asn	Thr	Arg	Val	Ala	Pro	Tyr	Asn	Ser	Ile	Ala	Tyr	Ile	
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aca	ttt	ggt	gga	tct	agc	tgc	act	gga	aca	ctc	att	gct	cca	aac	aaa	384
Thr	Phe	Gly	Gly	Ser	Ser	Cys	Thr	Gly	Thr	Leu	Ile	Ala	Pro	Asn	Lys	
				30					35					40		
ata	ttg	aca	aac	gga	cac	tgc	gtc	tac	aat	aca	gcc	aca	aga	agt	tat	432
Ile	Leu	Thr	Asn	Gly	His	Cys	Val	Tyr	Asn	Thr	Ala	Thr	Arg	Ser	Tyr	
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agt	gca	aaa	ggg	tct	gtc	tac	cca	ggc	atg	aat	gac	agc	acg	gct	gtg	480
Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala	Val	
		60					65				70					
aac	ggc	tca	gca	aac	atg	acc	gaa	ttc	tat	gta	cca	agc	gga	tat	atc	528
Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr	Ile	
	75					80					85					
aac	acg	ggg	gcg	agt	caa	tat	gat	ttt	gcc	gtc	att	aaa	aca	gat	acg	576
Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp	Thr	
90					95					100					105	
aac	att	gga	aat	acg	gtc	ggc	tat	cgc	tct	att	cgt	caa	gtg	aca	aat	624
Asn	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Arg	Ser	Ile	Arg	Gln	Val	Thr	Asn	
				110					115				120			
cta	aca	ggt	aca	acg	att	aaa	att	tct	gga	tat	cca	ggt	gat	aaa	atg	672
Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys	Met	
			125					130					135			
aga	tcg	act	ggc	aaa	gtg	tca	caa	tgg	gaa	atg	tca	ggt	cca	gtc	acg	720
Arg	Ser	Thr	Gly	Lys	Val	Ser	Gln	Trp	Glu	Met	Ser	Gly	Pro	Val	Thr	
		140					145					150				
aga	gaa	gat	acg	aat	ctc	gca	tac	tat	acg	atc	gat	aca	ttt	agc	gga	768
Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Thr	Ile	Asp	Thr	Phe	Ser	Gly	
	155					160					165					
aac	tct	ggc	tct	gcg	atg	cta	gat	cag	aac	caa	caa	atc	gtc	ggg	gtc	816

Asn 170	Ser	Gly	Ser	Ala	Met 175	Leu	Asp	Gln	Asn	Gln 180	Gln	Ile	Val	Gly	Val 185	
cat His	aat Asn	gcg Ala	ggt Gly	tat Tyr 190	tca Ser	aat Asn	gga Gly	acg Thr	atc Ile 195	aac Asn	ggt Gly	gga Gly	cca Pro	aaa Lys 200	gcg Ala	864
act Thr	gct Ala	gcc Ala	ttt Phe 205	gtt Val	gaa Glu	ttt Phe	atc Ile	aac Asn 210	tat Tyr	gcg Ala	aag Lys	gcg Ala	caa Gln 215			906

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 -70 -65 -60
 Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40
 Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25
 Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10
 Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5
 Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25
 Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
 30 35 40
 Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
 45 50 55
 Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
 60 65 70
 Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
 75 80 85
 Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
 90 95 100 105
 Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
 110 115 120
 Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
 125 130 135
 Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
 140 145 150
 Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
 155 160 165
 Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
 170 175 180 185

His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
 190 195 200
 Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
 205 210 215

<210> 13
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 <213> Bacillus subtilis IS75

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 <223> pro-peptide (103) ... (279)

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 gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca 96
 Val Leu Cys Leu Ala Leu Ala Ala Val Ser Phe Gly Val Pro Ala
 -75 -70 -65

 aaa gcg gca gag aac ccg caa act tct gta tcg aat acc ggt aaa gaa 144
 Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
 -60 -55 -50

 gct gat gct acg aaa aac caa acg tca aaa gca gat cag gtt tcc gcc 192
 Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
 -45 -40 -35 -30

 cct tat gag gga acc gga aaa aca agt aaa tcg tta tac ggc ggc caa 240
 Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
 -25 -20 -15

 acg gaa ctg gaa aaa aac att caa acc tta cag cct tcg agc att atc 288
 Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
 -10 -5 -1 1

 gga act gat gaa cgc acc aga atc tcc agc acg aca tct ttt cca tat 336
 Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr
 5 10 15

 aga gca acc gtt caa ctg tca atc aag tat ccc aac act tca agc act 384
 Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
 20 25 30 35

 tat gga tgt acc gga ttt tta gtc aat cca aat aca gtc gtc acg gct 432
 Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
 40 45 50

 gga cat tgt gtg tac agc cag gat cat gga tgg gct tcg acg ata acc 480
 Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
 55 60 65

gcc gcg ccg ggc cgc aat ggt tcg tca tat ccg tac ggt act tat tca 528
 Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser
 70 75 80
 ggc acg atg ttt tac tcc gtc aaa gga tgg acg gaa agc aaa gac acc 576
 Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
 85 90 95
 aac tat gat tac gga gct att aaa tta aac ggt tct cct gga aac acg 624
 Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
 100 105 110 115
 gtt ggc tgg tac ggc tac cgg act aca aac agc agc agt ccc gtg ggc 672
 Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
 120 125 130
 ctt tcc tcg tca gtg aca gga ttc cca tgt gac aaa acc ttt ggc acg 720
 Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
 135 140 145
 atg tgg tct gat aca aag ccg att cgc tcc gct gaa acg tat aag ctg 768
 Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
 150 155 160
 acc tat aca acc gat acg tac ggc tgc caa agc ggc tcg cct gtt tat 816
 Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
 165 170 175
 cga aac tac agt gat aca ggg cag aca gct att gcc att cac acg aac 864
 Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
 180 185 190 195
 gga gga tcg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc 912
 Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
 200 205 210
 aac aat att caa tat tgg gca aat caa 939
 Asn Asn Ile Gln Tyr Trp Ala Asn Gln
 215 220

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 <211> 313
 <212> PRT
 <213> Bacillus subtilis IS75

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 -75 -70 -65
 Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
 -60 -55 -50
 Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
 -45 -40 -35 -30
 Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
 -25 -20 -15
 Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
 -10 -5 -1 1
 Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr

5 10 15
 Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
 20 25 30 35
 Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
 40 45 50
 Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
 55 60 65
 Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser
 70 75 80
 Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
 85 90 95
 Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
 100 105 110 115
 Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
 120 125 130
 Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
 135 140 145
 Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
 150 155 160
 Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
 165 170 175
 Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
 180 185 190 195
 Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
 200 205 210
 Asn Asn Ile Gln Tyr Trp Ala Asn Gln
 215 220

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 <212> DNA
 <213> Bacillus intermedius

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<220>
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 <222> (265)..(909)

<220>
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 <222> (1)..(78)
 <223> pro-peptide (79) ... (264)

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 -85 -80 -75
 gct tta agt gtg cct agt ttt gcc cat gcc aca tcg gat tca gta cta 96
 Page 18

Ala	Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Thr	Ser	Asp	Ser	Val	Leu	
		-70					-65					-60				
acg	tct	gat	tat	gac	atg	gtg	act	tct	gat	gga	aag	gtg	atc	tct	tca	144
Thr	Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser	
	-55					-50				-45						
agt	gat	ttc	cac	aat	gat	acg	aaa	tcc	ccc	tca	tcc	ttt	gac	aaa	gtg	192
Ser	Asp	Phe	His	Asn	Asp	Thr	Lys	Ser	Pro	Ser	Ser	Phe	Asp	Lys	Val	
-40					-35				-30						-25	
gat	gat	ctt	tct	tct	act	tct	ggc	gaa	aaa	gta	aaa	cca	ctc	tca	aaa	240
Asp	Asp	Leu	Ser	Ser	Thr	Ser	Gly	Glu	Lys	Val	Lys	Pro	Leu	Ser	Lys	
				-20				-15						-10		
tat	tta	aaa	gac	ttt	caa	aca	aaa	gtc	gtc	att	gga	gac	gat	gga	ada	288
Tyr	Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Arg	
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aca	aaa	gta	gca	aac	aca	aga	gtg	gca	cca	tat	aat	tca	att	gct	tat	336
Thr	Lys	Val	Ala	Asn	Thr	Arg	Val	Ala	Pro	Tyr	Asn	Ser	Ile	Ala	Tyr	
	10					15					20					
att	aca	ttt	ggc	ggc	tca	agc	tgc	acg	ggg	aca	ctc	att	gcc	cct	aac	384
Ile	Thr	Phe	Gly	Gly	Ser	Ser	Cys	Thr	Gly	Thr	Leu	Ile	Ala	Pro	Asn	
25					30				35						40	
aaa	att	ttg	aca	aac	ggg	cac	tgc	gtg	tac	aat	aca	gca	tcg	aga	agt	432
Lys	Ile	Leu	Thr	Asn	Gly	His	Cys	Val	Tyr	Asn	Thr	Ala	Ser	Arg	Ser	
				45				50						55		
tat	agt	gca	aaa	gga	tcg	gtg	tat	cca	ggc	atg	aac	gat	agt	aca	gcg	480
Tyr	Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala	
			60					65					70			
gtg	aat	ggc	tca	gca	aac	atg	acg	gag	ttc	tat	gta	cca	agc	gga	tat	528
Val	Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr	
		75				80						85				
atc	aat	aca	ggc	gcg	agc	caa	tat	gat	ttt	gcc	gtg	atc	aaa	aca	gat	576
Ile	Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp	
	90					95					100					
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Asn	Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys	
				125					130					135		
atg	ada	tcg	act	ggc	aag	gtg	tcg	cad	tgg	gag	atg	tca	ggt	tct	gtg	720
Met	Arg	Ser	Thr	Gly	Lys	Val	Ser	Gln	Trp	Glu	Met	Ser	Gly	Ser	Val	
			140					145					150			
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Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Thr	Ile	Asp	Thr	Phe	Ser	
		155					160					165				
gga	aat	tca	ggc	tca	gcg	atg	cta	gat	caa	aat	cad	caa	atc	gtt	ggg	816
Gly	Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly	
	170					175					180					
gtt	cat	aac	gca	ggg	tat	tca	aac	gga	acg	att	aat	ggc	ggt	cca	aaa	864
Val	His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys	
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-5 -1 1 5
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
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Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
25 30 35 40
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
45 50 55
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
60 65 70
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
75 80 85
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
90 95 100
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
105 110 115 120
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
125 130 135
Met Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Ser Val
140 145 150
Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser
155 160 165
Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
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